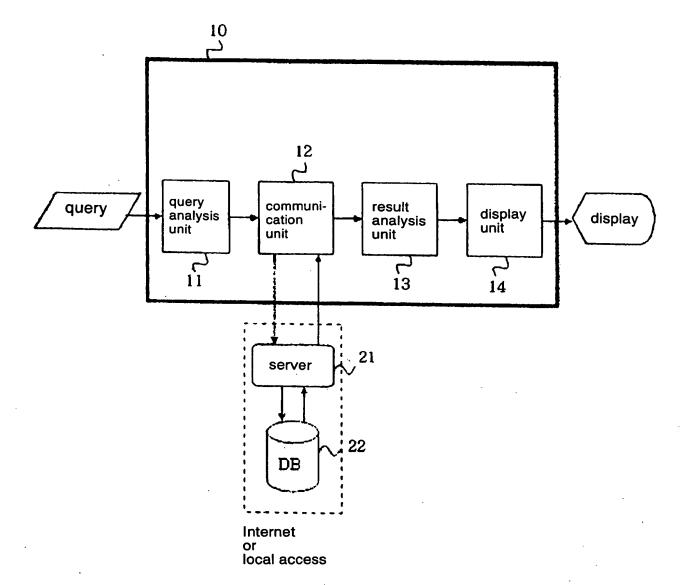
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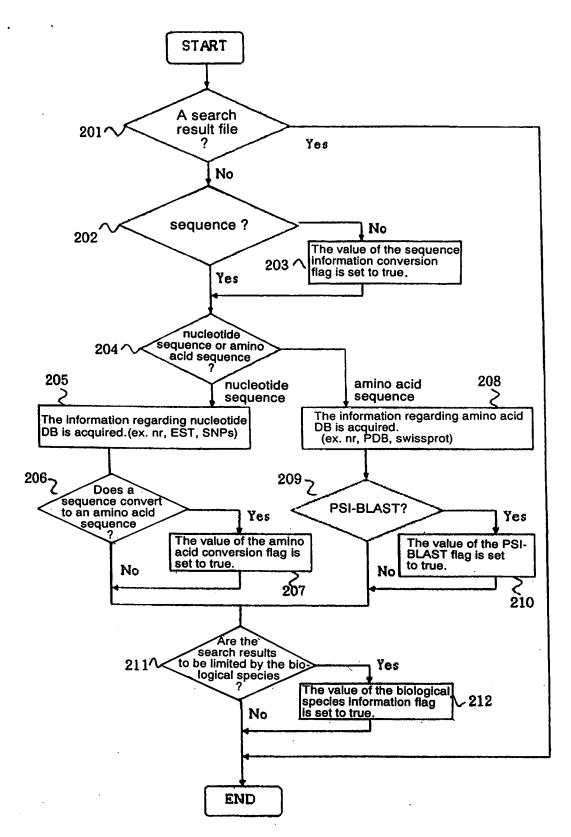
∘Fig. 1



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Fig. 2



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Fig. 3

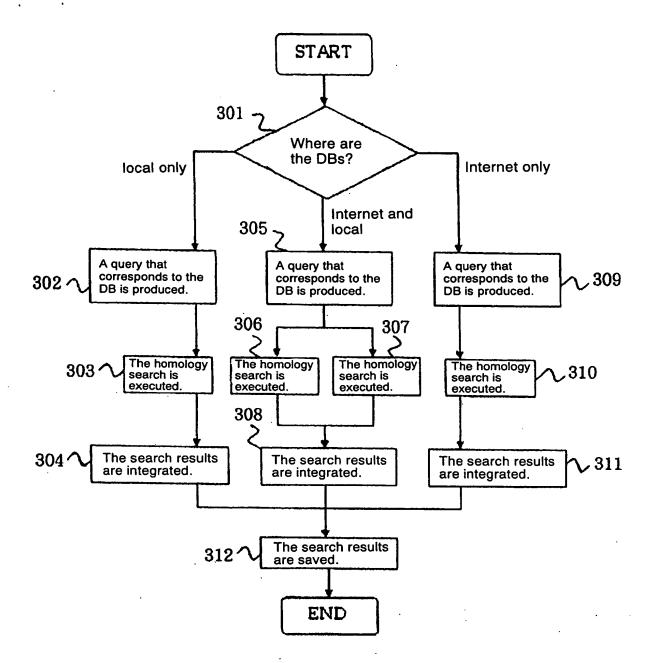
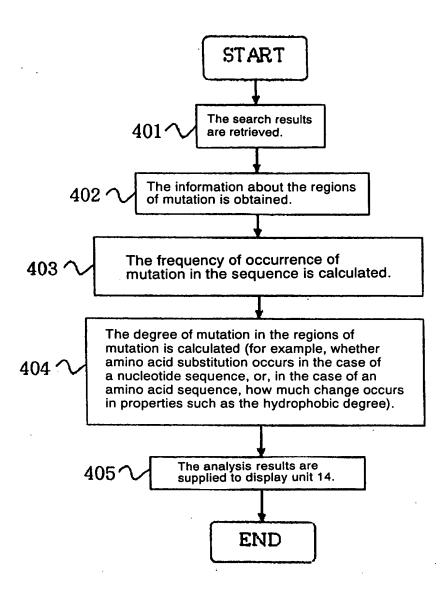


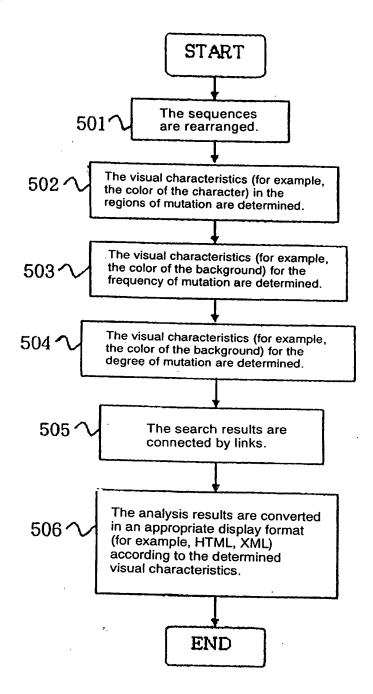
Fig. 4



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Fig. 5



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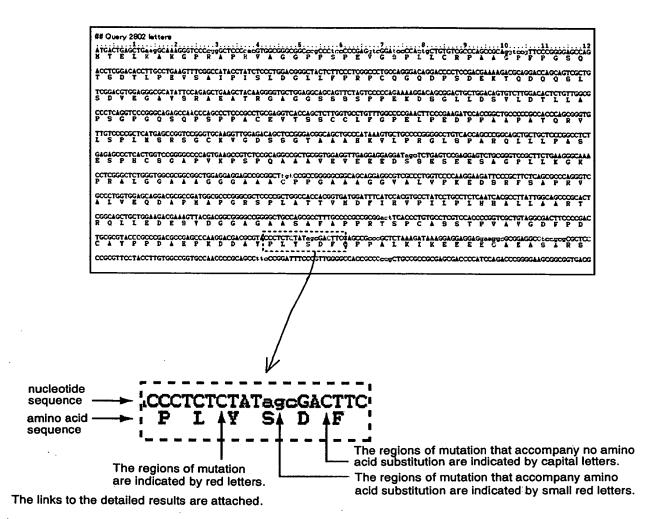
Fig. 6

Blast Auto Submition Form

If you submit, your q	nuery send to NCBI BLAST, and parse results.	<u> </u>
Enter your Query		<u>.</u>
or Enter Query File	Ref	
Choose database	Human nr W Human EST W Human SNPs	
Limit by entrez query	select from: Homo sapiens [ORGN]	
Display translated codon	☑check this out, ex.)query is promoter	
	bmit To clear the form Clear	***************************************
Blast Result Parser	Form	· · · · · · · · · · · · · · · · · · ·
Blast Result Parser	Form	
Blast Result Parser If you submit, parse	Form	· · · · · · · · · · · · · · · · · · ·
Blast Result Parser If you submit, parse Enter your Query	Form BLAST Result.	
Blast Result Parser If you submit, parse Enter your Query or Enter Query File	Form BLAST Result. [Ref.,:::]	

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· Fig. 7



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Fig. 8

ALIGNMENTS

			
gnl dbSNP re2008112 at gi 35651 emb X51730.1 BSPREC at gi 4102792 gb AF016381.1 AF016381 at gi 4505766 ref NM at gi 189934 gb M15716.1 HUMPGRR at gi 22759951 dbj AB085844.1 at gi 22759949 dbj AB085844.1 at gi 2278870 dbj AB085683.1 at gi 22759947 dbj AB085843.1 at gi 22759947 dbj AB085843.1 at gi 22759947 dbj AB085843.1 at	tgactgago tgaaggcaaa tgactgago tgallggcaaa tgactgago tgaaggcaaa	gggtccccllg gctcccllacg gggtccccgg gctcccacg gggtccccgg gctcccacg gggtccccgg gctcccacg gggtccccgg gctcccaca gggtccccgg gctcccaca gggtccccgg gctcccaca gggtccccgg gctcccaca gggtccccgg gctcccaca gggtccccgg gctccccaca	taleadacia contector palacia c
	•		
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	•		
gi 19692498 emb AI709143.1 AI709143 tau gi 15938608 gb BI827058.1 BI827058 tau gi 15938608 gb BI827058.1 BI832037 gi 22921092 gb BI832037.1 BI832037 gi 22921092 gb BI832037.1 BI832037 gi 22921092 gb BU570792.1 BU570792 tau gi 24718432 gb C388844.1 C3388844 tau gi 24117946 gb BU929216.1 BU929216 tau gi 14002248 gb BC723061.1 BC723061 tau gi 14002248 gb BC723061.1 BC723061 tau gi 9868409 dbj AV647486.1 AV647486 tau gi 9868409 dbj AV647485.1 AV647483 tau gi 9868443 dbj AV647489.1 AV647483 tau gi 9868443 dbj AV647489.2 AV647489 tau gi 9868443 dbj AV647489.2 AV647489 tau gi 9868694 gb AI636264.1 AI636264 tau gi 9868694 dbj AV647680.1 AV647680 tau gi 9868694 dbj AV647680.1 AV647680 tau gi 9868694 dbj AV647680.1 AV647680 tau gi 9988698 gb BC446111.1 BC446111 Bau gi 9988694 dbj AV647680.1 BC546769 tau gi 1001479 dbj AA076157.1 AA0761557 gi 9775354 gb BE546709.1 BE546709 tau gi 15263605 gb BI438915.1 BI438915 tau gi 15263605 gb BI4382009.1 AV951606 tau gi 15263462 gb AV951606.1 AV951606	acttatyty ctggaagaaa acttatyty ctggaagaa	tga igcatc it gataaaa tga tgcatc it gataaaa	togcagaaa aaactgooca togcagaaa aaactgooca togcagaaa aaactgooca togcagaaa aaactgooca togcagaaa aaactgooca tog agaaa aaactgooca

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. Fig. 9

Blast Auto Submition Form

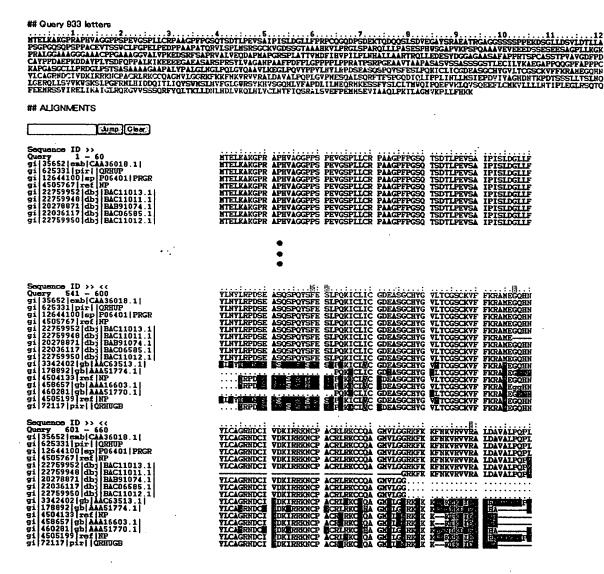
If you submit, your	query send to NCBI BLAST, and parse results.	~
Enter your Query		
or Enter Query File	Ref	
Choose database	nr 🔛	
Limit by entrez query	select from: (none)	
PSI BLAST iteration	1 means standard blastp	
To submit the query. S	ubmit: To clear the form Clear	
Blast Result Parse	r Form	
If you submit, parse	BLAST Result.	
Enter your Query		
or Enter Query File	Ref.	
<u>.</u> -		
Enter Blast Result File	Ref.	
Enter Blast Result File	Ref	
Enter Blast Result File	Ref.	
To submit the query S	ubmit. To clear the form Olean	

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"Fig.' 10



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Fig. 11

0 .-2 2 -3 0 2 -2 -3 -2 -3 -12 -2 5 -3 -3 0 -3 -11 -2 -3 -3 -2 -2 8 -2 0 -2 -3 -3 -1 -2 2 -3 -2 2 0 -3 -2 -1 -2 -2 -2 -3 -1 -3 5 -1 0 -2 -3 -2 1 2 -1 5 0 -2 -1 -3 -3 -3 -3 0 -1 -2 -2 -3 -3 0 - 1 - 2-2 -2 T -2 -1 -1 -1 -1 -2 -1 5 -2 -3 -2 -2 -3 -2 -3 -1 -2 11 -2 -3 2 -1 -1 -2 -1 3 -3 -2 -2 0 -3 -3 -3 -1 -2 -3 -3 3 1 -2 1 -1 -2 -2 0 -3 -4 0 -3 -3 -2 2 -1 -2 0 -3 -3 -3 -1 -1 -1 -1 -2 0 -2 -1 -1 -1 -1 -1 -4

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Fig. 12

```
IMAGE: 4165725, mRNA, complete cds
       Length = 2681
Score = 44.1 bits (22), Expect = 1.1 Identities = 85/106 (80%)
Strand = Plus / Plus
Score = 44.1 bits (22), Expect = 1.1
Identities = 25/26 (86%)
Strand = Plus / Plus
☑>gi|22775806|gb|AY049076.1| ☐☐ Mus musculus anion exchanger SLC26A6a mRNA, complete cds
       Length = 2552
Score = 44.1 bits (22), Expect = 1.1 Identities = 85/106 (80%)
Strand = Plus / Plus
Score = 44.1 bits (22), Expect = 1.1
Identities = 25/28 (98%)
Strand = Plus / Plus
Query: 1805 tstactttsccaatsctsasctctac 1880
SbJct: 1878 tgtacttcgccaatgctgagctctac 1704
```

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Fig. 13

